

FIG. 1A

Sequence I

-72 AGGAAACCTGCC

-60 ATGGCCTCCTGGTGAGCTGTCTCATCCACTGCTGCTGCTCCTCTCCAGATACTCTGACCC

1 M D P L G A A K P Q W P W R R C L A A L

1 ATGGATCCCCCTGGGTGAGCAAGCAAGCAATGGCCATGGCGCCGCTGTCTGGCCGCACTG

21 L F O L L V A V C F F S Y L R V S R D D

61 CTATTTTCAGCTGCTGGTGGCTGTGTGTTTCTTCTCTACCTGCGTGTGTCCGAGACGAT

41 A T G S P R A P S G S S R Q D T T P T R

121 GCCACTGGATCCCCCTAGGGCTCCAGTGGTCCCTCCGACAGGACACCACTCCACCCGC

61 P T L L I L L W T W P F H I P V A L S R

181 CCCACCCTCCTGATCCTGCTATGACATGGCCTTCCACATCCCTGTGGCTCTGTCCCGC

81 C S E M V P G T A D C H I T A D R K V Y

241 TGTTACAGAGATGGTGCCCGCACAGCCGACTGCCACATCACTGCCGACCGCAAGGTGTAC

101 P Q A D T V I V H H W D I M S N P K S R

301 CCACAGGCAGACACGGTCACTCGTGACCACTGGGATATCATGTCCAACCTAAGTACCGC

121 L P P S P R P Q G Q R W I W F N L E P P

361 CTCCCACCTTCCCCGAGGCCGAGGGCAGCGCTGGATCTGGTTCAACTTGGAGCCACCC

141 P N C Q H L E A L D R Y F N L T M S Y R

421 CCTAACTGCCAGCACCTGGAAGCCCTGGACAGATACTTCAATCTCACCATGTCTCTACCGC

161 S D S D I F T P Y G W L E P W S G Q P A

481 AGGACTCCGACATCTTCACGCCCTACGGCTGGTGGAGCCGTGGTCCGGCCAGCCTGCCA

181 H P P L N L S A K T E L V A W A V S N W

541 CACCACCGCTCAACCTCTCGGCCAAGACCGAGCTGGTGGCCTGGGCGGTGTCCAACTGG

1261 GACCTCGCCTGTTGGGGACCTCACCTTGC1GGGGACCTCACCTCGCTG

1321 TGGAGGCTGCACCTACTGAGGATGTGGCGGTCTGGGGACCTTACCTGCTGGGACCTGCTC
1381 CCAGAGACCTTGCCACACTGAATCTACCTGCTGGGACCTCACCTGGAGGGCCCTGGG
1441 CCCTGGGAACTGGCTTACTTGGGGCCCCACCCGGGAGTGATGGTTCTGGCTGATTGTT
1501 TGTGATGTTAGCCGCTGTGAGGGGTGCAGAGAGATCATCAGGCACGGTTTCCAGA
1561 TGTAATACTGCAAGGAAAAATGATGACGTGTCTCCTCACTCTAGAGGGTTGGTCCCATG
1621 GGTTAAGAGCTCACCCAGGTTCTCACCTCAGGGGTTAAGAGCTCAGAGTTCAGACAGGT
1681 CCAAGTTCAAGCCAGGACCACTTATAGGGTACAGGTGGGATCGACTGTAAATGAGG
1741 ACTTCTGGAACATTCCAAATATTCTGGGGTTGAGGGAATTGCTGCTGTCTACAAAATGC
1801 CAAGGTGGACAGCGCTGTGGCTCAGCCCTGTAAATTCAGCACTTTGGGAGGCTGAGGT
1861 AGGAGGATTGATTGAGGCCAACAGTTAAAGACCAGCCTGGTCAATATAGCAAGACCACGT
1921 CTCTAAATAAAAAATAATAGCGCGCCAGGAAAAAATAAAAAA

FIG. 1C

FIG. 2A

Sequence II

-276 CCTTCCCTTGAGACTCTTCTTGGAATGAGAAGTAC
CGATTCTGCTGAAGACCTCGCGCTCTCAGGCTCTGGGAGTTGGAACCCCTGTACCTTCCTT
TCCTCTGCTGAGCCCTGCCTCCTTAGGCAGGCCAGAGCTCGACAGAACTCGGTTGCTTTG
CTGTTTGCTTTGGAGGGAACACAGCTGACGATGAGGCTGACTTTGAACCTCAAGAGATCTG
CTTACCCAGTCTCCTGGAATTAAGGCCCTGTACTACATTTGCCTGGACCTAAGATTTTC
1 M I T M L Q D L H V N K I S M S R S K S
1 ATGATCACTATGCTTCAAGATCTCCATGTCAACAAGATCTCCATGTCAAGATCCAAGTCA
21 E T S L P S S R S G S Q E K I M N V K G
61 GAAACAAGTCTTCCATCCTCAAGATCTGGATCACAGGAGAAAATAATGAATGTCAAGGGA
K V I L L M L I V S T V V V V F W E Y V
AAAGTAATCCTGTTGATGCTGATTGTCTCAACCGTGGTGTGTCGTGTTTGGGAATATGTC
N R I P E V G E N R W Q K D W W F P S W
AACAGAAATCCAGAGGTTGGTGAGAACAGATGGCAGAAAGGACTGGTGTCCCAAGCTGG
F K N G T H S Y Q E D N V E G R R E K G
TTTAAATAATGGGACCCACAGTTATCAAGAAGACAAACGTAGAAGGACGGAGAGAAAAGGCT
R N G D R I E E P Q L W D W F N P K N R
AGAAATGGAGATCGCATTTGAAGAGCCTCAGCTATGGGACTGGTTCAATCCAAAGAACCCGC
P D V L T V T P W K A P I V W E G T Y D
CCGGATGTTTGTGACAGTGACCCCGTGGAGGCCCGGATTTGTGGGAAGGCCACTTATGAC

FIG. 2B

141	T A L L E K Y Y A T Q K L T V G L T V F
421	ACAGCTCTGCTGGAAGTACTACGCCACACAGAACTCACTGTGGGCTGACAGTGTTT
161	A V G K Y I E H Y L E D F L E S A D M U
481	GCTGTGGAAAGTACATTGAGCATTACTTAGAGACTTTCTGGAGTCTGCTGACATGTAC
181	F M V G H R V I F Y V M I D D T S R M P
541	TTCATGGTTGGCCATCGGTCATATTTTACGTCATGATAGACGACACCTCCCGGATGCCT
201	V V H L N P L H S L Q V F E I R S E K R
601	GTCGTGCACCTGAACCTCTACATTCCTTACAAGTCTTTTGAGATCAGTCTGAGAAGAGG
221	W Q D I S M M R M K T I G E H I L A H I
661	TGGCAGGATATCAGCATGATGGCATGAAGACCATTGGGGAGCACATCCTGGCCACATC
241	Q H E V D F L F C M D V D Q V F Q D N F
721	CAGCAGAGGTCGACTTCCTCTCTGTCATGGACGTGGATCAAGTCTTTCAAGACAACTTC
261	G V E T L G Q L V A Q L Q A W W Y K A S
781	GGGTGGAAACTCTGGCCAGCTGGTAGCACAGCTCCAGGCCCTGGTGTTACAAGGCCAGT
281	P E K F T Y E R R E L S A A Y I P F G E
841	CCCGAGAAGTTCACCTATGAGAGCGCGGAACCTGTGGCCGCGTACATTCCATTCCGGAGAG
301	G D F Y Y H A A I F G G T P T H I L N L
901	GGGGAATTTTACTACACGGGCCATTTTGGAGGAACGCCCTACTCACATTCTCAACCTC
321	T R E C F K G I L Q D K K H D I E A Q W
961	ACCAGGAGTGCTTTAAGGGGATCCTCCAGGACAAGAAACATGACATAGAAGCCAGTGG
341	H D E S H L N K Y F L F N K P T K I L S
1021	CATGATGAGGCCACCTCAACAAATACTTCCTTTTCAACAAACCCACTAAATCCTATCT

FIG. 2C

361 P E Y C W D Y Q I G L P S D I K S V K V
1081 CCAGAGTATTGCTGGGACTATCAGATAGGCCTGCCCTTCAGATATTAAAGTGTCAAGGTA
381 A W Q T K E Y N L V R N N V *
1141 GCTTGGCAGACAAAAGAGTATAATTGGTTAGAAATAATGTCCTGACTTCAAATTGTGATG
1201 GAAACTTGACACTATTCTAACCA

FIG. 2C

Sequence III

10	20	30	40	50	60
GAATTCCATCGTGGCAAGGCAGCCCTGAATGGATGATGTAACCTGGGGTCTTCAATGG					
70	80	90	100	110	120
AGGGCCAGACTCCTGGGTCTAGGGGATGAGGGGAGGGAGGATCGGGTTAGCTGGGACCCA					
130	140	150	160	170	180
GGTGAAGGGGCTGGGGCCACATTCCTGAGTCTCAGAGAGAAGGATCTGGGGTCTCAA					
190	200	210	220	230	240
GCACCTGAGTCGGAGGGAGGGGTGCTGGGCTCCTGGAAAAAACCACTCTTGGACCAT					
250	260	270	280	290	300
CTATGCAGATCAGCAGAACAAAGAGAAATTTCTGGCCCCCATCTGAATTTCTAAGTTGG					
310	320	330	340	350	360
GGGAGGGCGTGATCTGACACTGAGGTTCTTGATCCTCAGCAAGCGGCAATTGCTGTA					
370	380	390	400	410	420
TGAAAGAAGCGACCGCATCTGAGACACAAGTATCCTGCCTTGGAGCCTCTCACCTGGCC					
430	440	450	460	470	480
GTGGGCCAACCTCAACCTCATCTGTCCCTGCTCAGATGCTCAGACCCCTGGACATCCCAGC					
490	500	510	520	530	540
CTCCTCCTCCTGATGCAATCCTGGTGTCTTTTCCACAGAGAAGCCATCCCAGGCCAG					
550	560	570	580	590	600
GCAGGTGCTCCTGAAATAACCTGGGGGAGGGGTGGCTGAAAGTCCCTGACTGGAGTTGG					
610	620	630	640	650	660
CAGCCAAGCCAGGCCCTGGAGTGGGACCCAGAGGGAAGACAGGTTGGCTAATTTCCCTGG					

FIG. 3A

FIG. 3B

FIG. 3B

670 680 690 700 710 720
AGCCCCAAGGGTGCAAGGTAGGCCCTTCTGTGCTGAGGGAGGAGGCTGGGCTCTGG
730 740 750 760 770 780
ACTCCTGGGTCTGAGGGAGGAGGGGTGGGGCCCTGGACTCCTGGGTCTGAGGGAGGAGG
790 800 810 820 830 840
GTCTGGCCCTGTACTCCTGGATCTGAGGGAGGGGCTGGGGAACCTTGGGCTCCTGGGT
850 860 870 880 890 900
CTGAGGGAGGAGGAGCTTTGGTCTGGACTCCTGGGTCTGAGGGAGTAGGGCTAGGGAT
910 920 930 940 950 960
CTGGACTCGTGGGTGTGAGGAAGGAGGGGCTGGGTCTGGACTCCTGGGTCTGAGGAAG
970 980 990 1000 1010 1020
GAGGGCAGGGGCTTGGACTCCTGGGTCTGAGGAAGGAGGGCCGGAGCCTGGACTCC
1030 1040 1050 1060 1070 1080
TAAGTCTGAGGGAGGGTCTGGGGCCCTGGACTGCTGGGTGTGAGCACAAAGGTCTGG
1090 1100 1110 1120 1130 1140
GTGCTGGGAGTCCCGAGCCTGGGAGATGATGGTTAACTTCTGGGAATCAAGTCAAAC
1150 1160 1170 1180 1190 1200
CCTGAGTCTTTGACATTGATGTATCTTGAATGGGAGGTCAGTCTGTGGGAAGGATTAC
1210 1220 1230 1240 1250 1260
CCAGGTGCCGAGGCAAGAGACTGAAGGCACAACTGTTTCAGTATAATAAGAAAATAGT
1270 1280 1290 1300 1310 1320
TAGAATAAGAAATAGTTATCATACAAATTAGATATAGAGATGATCATGGACAGTATCAATC

1330 1340 1350 1360 1370 1380
ATTAGTGAAACATTATTAATCATTAGCTATTACTTTTATTCTTTGTTGATAACTAATA
1390 1400 1410 1420 1430 1440
TAACCAGGAACAACCGGTGGGTATAGGGTCAGGTACTGAAGGGACATTGTGAGAGTGA
1450 1460 1470 1480 1490 1500
CCTAGAAGGCAAGAGGTGAGCCTTCTGTCAACCCGGCATAAGGGCCTCTTGAGGGCTCCT
1510 1520 1530 1540 1550 1560
TGGTCAAGGGGAACGCCAGTGTCTGGGAAGGCACCCGTTACTCAGCAGACCACGAAAGG
1570 1580 1590 1600 1610 1620
GAATCTCCTTTTCTTGGAGGAGTCAGGGAACACTCTGCTCCACCAGCTTCTTGTGGGAGG
1630 1640 1650 1660 1670 1680
CTGGGTATTATCTAGGCCCTGCCCGCAGTCATCCTGCTGTGCTGTGCTTCAATGGTCACGC
1690 1700 1710 1720 1730 1740
TCCTTGTCCTCTTGCAATTTTCTCCCGTACTCCTGGTCCCTTTTGAAGTTCGTAGTAGA
1750 1760 1770 1780 1790 1800
TAGCGGTAGAGAAATAGTGAAAGCCTTTTCTTTTGTGAGGCGGAGTCTCGCTC
1810 1820 1830 1840 1850 1860
TGTCGCCAGGCTGGAGTGCAGTGGCGTGATCTCGGCTCACTGCAATCTCCGCCCTCCTGG
1870 1880 1890 1900 1910 1920
GTTACACCAATTCTCCTGCCCTCACCCCTCCCAATAGCTAGGACTACAGGCGCCCTCCACC
1930 1940 1950 1960 1970 1980
ACGCGCCCGGATAATTTTGTGATTTTGTAGTAGACAGGGTTTCAACCGTGTAGCCAGG

FIG. 3C

FIG. 3D

1990 2000 2010 2020 2030 2040
ATGGCCTCCACCTCCTGACCTTGTGATCCGCCCGCCTCAGCCTCCCAAAGTGCTGGGATT

2050 2060 2070 2080 2090 2100
ACAGCGGTGAGCCACCGCGCCCGCGAAATAGTGAAGTCTTAAAGTCTTTGATCTTTC

2110 2120 2130 2140 2150 2160
TTATAAGTGCAGAGAAGAAAACGCTGACATATGCTGCTTCTCTTCTGCTTCGGCTGCC

2170 2180 2190 2200 2210 2220
TAAAGGGAAGGGCCCCCTGTCCCATGATACGTGACTTGCTTGACCTTATCAGTCATTT

2230 2240 2250 2260 2270 2280
GGACGACTCACCCCTCCTTATCCTGCCCCCCTTGCTTGATACAATAAATATCAGCGCG

2290 2300 2310 2320 2330 2340
CCAGCCATTGCGGGCCACTACCGGCTCTCTGGCTCTTGATGGTAGTGTCCTCCCGGGCCC

2350 2360 2370 2380 2390 2400
AGCTGTTTCTCTTTATCTCTTTGTCTTTGTCTTTATTTCTTACAAATCTCTCTCTCCT

2410 2420 2430 2440 2450 2460
CACAGGGAAGAACACCCACCCGCAAGCCCCGTAGGGCTGGACCTACGTTAGCCTGCC

2470 2480 2490 2500 2510 2520
CTGCTCGGGTTGGCGATGCTGGAGGTGGGCTTGAGCCAGAGAAAATGCTTAAATTAGG

2530 2540 2550 2560 2570 2580
TGACAAAGCGGCAGAGGCCCTTGTCTCTGGCGCGGCAGCCACGGCCCCCGCTGACGGCG

2590 2600 2610 2620 2630 2640
TGGGAAACAGACCCCTGTTCCACTCCGGTCTCCAGCCCTTGGAAATGGTTGCCCTCGTGCAGT

2650 2660 2670 2680 2690 2700
GCAGGTCTGGAAAGTAGCAGTTTGGACGGGACCCTAGAAATCCCCAAAGAGTGACTA

2710 2720 2730 2740 2750 2760
GGGGCTGGGATTCTGGAATTTGAGTGTGGACGGTGAGCGGGGGGTGTGGGAGATCGGAG

2770 2780 2790 2800 2810 2820
ACCTTGGTGGGCGGGAGACACCTGCAGGCTGGAGGCCCTCGCGCGCTCCGGCGGCAGCC

2830 2840 2850 2860 2870 2880
TGGCAAAACAGGTTCTCCATCCCCCAGGAGGACGCGGCAGAGGGCGGACGATCGCTCCACT

2890 2900 2910 2920 2930 2940
CGCCGGGACCAAGGTGCGGGGGCCCTGCCAGCCGCTGGGGCGTGGCCAGGCTCGAAGCAC

2950 2960 2970 2980 2990 3000
CCAGGTGTCGGGGGCCGACTCTAAGCCCTGGCACCGGAAGAGAGAGGGCGCGGATTGGA

3010 3020 3030 3040 3050 3060
CCTCCCGGCTCCAGCATTGCAACTGGGCGCTCCGTCTCTGTGTCCACGCAATGATGCTGC

3070 3080 3090 3100 3110 3120
GGCTGCTCAGAAGCCAGGTAGCCTGCCCTGGGTGAAGCCTTCGCGCAGGTCAATGACGGG

3130 3140 3150 3160 3170 3180
GGGAGGGGCAGGGCGGGTCCCCCTGCATCCCCGATCTGGGAGCGGTGGGCCACAGGGC

3190 3200 3210 3220 3230 3240
CATCGCCTTAGCCCCCTGGCGCTGGGGCTCGGCGCCAAAGTACGGGGGGGTCCACCTTC

3250 3260 3270 3280 3290 3300
CAGCCATCCGCCCGGCCGGAGGGGACGCTGCGAGACTCCCGGGCGGCCCTCTCCT

FIG. 3E

FIG. 3F

3310 3320 3330 3340 3350 3360
TCCTCTCCTCCCAAGCCCTCGCTGCCAGTCCGGACAGGCTGCGGGAGGGAGGGCTGC

3370 3380 3390 3400 3410 3420
CGGGCCGGATAGCCGGACGCCCTGGCGTTCAGGGCGGCGGATGTGGCCTTGCTTTGCG

3430 3440 3450 3460 3470 3480
GAGGGTGGCTCCGGCCACGAAAGCGGACTGTGGATCTGCCACCTGCAAGCAGCTCGGC

3490 3500 3510 3520 3530 3540
TAAGTGGGACTGCCCCACTCAGTTGTTCTCTGGGACCCAGGAACAACCTCTCAGAACCA

3550 3560 3570 3580 3590 3600
GGAGGTGACCCCAACCTCTTCTCCAGGTCTTCTAAGGCCCTAGGAATCTCCGCCACC

3610 3620 3630 3640 3650 3660
TCCCCAGCCATTACTCCTCCAGGAACCAAGATGCTCTTCCGCTCCTGACCCCTCCAGCCT

3670 3680 3690 3700 3710 3720
CTCTTGTTTACTTGAACTATCGTTTCCCATCACCACTCTGTGGTGGATTTTGGCCCTC

3730 3740 3750 3760 3770 3780
ACAGACAGGTACTCCTGAGAAACAGGCTGGTGGAGAGTCCAGTATCAGCGGAACCTTASC

3790 3800 3810 3820 3830 3840
AGGAGGGGAGACTCGAGATTCTTTCAGGAAAGGTGTAGGAACCTGGACCCTTCTTTT

3850 3860 3870 3880 3890 3900
TTTTTTTTTTTTTTTAAAGACAGGTCCTCTCTGTGCGCAAGCTGGAGTGCAGTCAG

3910 3920 3930 3940 3950 3960
CGGTGCTATCGGGCTCATTTGTGAGCTCCGGGGATCCTCCCGCCTTAGCATCCGGGTAG

TOTAL 548860

3970 3980 3990 4000 4010 4020
CTGAGACCACAGACATGTGCCACCATGCCAAGCTAATTTTATTTTATTTTGGAGAC

4030 4040 4050 4060 4070 4080
GGAGTTTCACTCTTGTGCCAGGCTGGAGTGTAATGGCATGATCTCAGCTCACCGCAAC

4090 4100 4110 4120 4130 4140
TCCCCCCCCGGGTTTCAGGCGATTCTCCTGCCCTCAGCCTCCCGAGTGGCTGGGATTACA

4150 4160 4170 4180 4190 4200
GGCATGCGCACCATGCCCCGGCTAATTTTGATTTTAAGTAGACAGGGTTTCTCCACG

4210 4220 4230 4240 4250 4260
TTGGTCAGGCTGGTCTCGAACTCCCAACCTCAGGTGATCCACCCACCTTGGCCTCCCAA

4270 4280 4290 4300 4310 4320
GTGCTGGGATTACAGGTGTGAGCCACCGCGCTGGCCCATGCCAAGCTAATTTTAAAT

4330 4340 4350 4360 4370 4380
TTTTTTGTAAGAGTGCTCTGTGCCCCAGGCTGATCTTGAACCTCCTGGGCTCAAGGGATCCT

4390 4400 4410 4420 4430 4440
CCCATCTCAGCCTCCCAATATGTCTGGGATTACAGGTGTGAGCCACAGTGCCAGCCAAAC

4450 4460 4470 4480 4490 4500
CATGGCTATCTTGAAACCACTTGCTTCCAGTCCCAATGCCCGAAATTCCAAGGCTCT

4510 4520 4530 4540 4550 4560
CATCCCTGAAACCTAGGACTCAGGCTCTCCCTACCTCAGCCCCAGGAGTCTAAACCTTTA

4570 4580 4590 4600 4610 4620
ACTTCCCTCTTCCCTGGGACTAAGGAGTGCTGCACCCAGGCGCCTCCCTTACCCACAT

FIG. 36

4630 4640 4650 4660 4670 4680
CCCTCCTCAGCCTCCCTCCTCAGCCTCAGTGCAATTGCTAATTGCGCTTTCTCCTCCCTG
4690 4700 4710 4720 4730 4740
CAGCCATGTGGCTCCGGAGCCATCGTCAGCTCTGCGCTTCTGCTAGTCTGTGTCC
MetTrpLeuArgSerHisArgGlnLeuCysLeuAlaPheLeuValCysValL
4750 4760 4770 4780 4790 4800
TCTCTGTAATCTTCTCCTCATATCCATCAAGACAGCTTCCACATGGCCTAGGCCTGT
euSerValIlePhePheLeuHisIleHisGlnAspSerPheProHisGlyLeuGlyLeus
4810 4820 4830 4840 4850 4860
CGATCCTGTGTCCAGACCGCCGCTGGTGACACCCCGAGTGGCATCTTCTGCGCTGCCGG
erIleLeuCysProAspArgArgLeuValThrProProValAlaIlePheCysLeuProG
4870 4880 4890 4900 4910 4920
GTACTGCGATGGGCCCCAACGCCCTCCTCTTCTGTCGCCAGCACCTGCTTCCCTCTCCG
lyThrAlaMetGlyProAsnAlaSerSerCysProGlnHisProAlaSerLeuSerg
4930 4940 4950 4960 4970 4980
GCACCTGGACTGTCTACCCCAATGGCCGGTTTGGTAATCAGATGGGACAGTATGCCACGC
lyThrTrpThrValTyrProAsnGlyArgPheGlyAsnGlnMetGlyGlnTyrAlaThrL
4990 5000 5010 5020 5030 5040
TGCTGGCTCTGGCCAGCTCAACGGCCCGCCGCTTATCCTGCGCTGCCATGCATGCCG
euLeuAlaLeuAlaGlnLeuAsnGlyArgArgAlaPheIleLeuProAlaMetHisAlaA
5050 5060 5070 5080 5090 5100
CCCTGGCCCCGGTATTCCGCATCACCTGCCCGTGGTGGCCCCAGAAAGTGACAGCCGCA
laLeuAlaProValPheArgIleThrLeuProValLeuAlaProGluValAspSerArgT
5110 5120 5130 5140 5150 5160
CGCCGTGGCGGAGCTGCAGCTTCACGACTGGATGTGGAGGAGTACGCGGACTTGAGAG
hrProTrpArgGluLeuGlnLeuHisAspTrpMetSerGluGluTyrAlaAspLeuArgA

FIG. 3H

5170 5180 5190 5200 5210 5220
ATCCTTCTGAAGCTCTCTGGCTTCCCTGCTCTTGGACTTCTTCCACCATCTCCGGG
spPropheLeuLysLeuSerGlyPheProCysSerTrpThrPhePheHisHisLeuArgG
5230 5240 5250 5260 5270 5280
AACAGATCCGACAGAGATTACCCCTGCACGACACCTTCGGGAAGAGCGCAGAGTGTGC
luGlnIleArgArgGluPheThrLeuHisAspHisLeuArgGluGluAlaGlnSerValL
5290 5300 5310 5320 5330 5340
TGGGTCAGCTCCGCTGGCCGCACAGGGACCGCCCGCACCTTGTGCGGCTCCACG
euGlyGlnLeuArgLeuGlyArgThrGlyAspArgProArgThrPheValGlyValHisV
5350 5360 5370 5380 5390 5400
TGCGCCGTGGGACTATCTGCAGGTTATGCCTCAGCGCTGGAAGGTGTGGTGGCGACA
alArgArgGlyAspTyrLeuGlnValMetProGlnArgTrpLysGlyValValGlyAsps
5410 5420 5430 5440 5450 5460
GCGCCTACCTCCGGCAGGCCATGGACTGGTTCCGGGCACGGCACGAAGCCCCGTTTCG
erAlaTyrLeuArgGlnAlaMetAspTrpPheArgAlaArgHisGluAlaProValPheV
5470 5480 5490 5500 5510 5520
TGGTCACCAAGCAACGGCATGGAGTGGTGTAAAGAAACATCGACACCTCCAGGGCGATG
alValThrSerAsnGlyMetGluTrpCysLysGluAsnIleAspThrSerGlnGlyAspV
5530 5540 5550 5560 5570 5580
TGACGTTTGCTGGCGATGGACAGGAGGCTACACCGTGGAAAGACTTTGCCCTGCTCACAC
alThrPheAlaGlyAspGlyGlnGluAlaThrProTrpLysAspPheAlaLeuLeuThrG

FIG. 31

5590 5600 5610 5620 5630 5640
AGTGCAACACACACATTATGACCATTGGCACCTTCGGCTTCTGGGCTGCCTACCTGGCTG
InCysAsnHisThrIleMetThrIleGlyThrPheGlyPheTrpAlaAlaTyrLeuAlaG
5650 5660 5670 5680 5690 5700
GCGGAGACACTGTCTACCTGGCCAACTTCACCCCTGCCAGACTCTGAGTTCTCTGAAGATCT
lyGlyAspThrValTyrLeuAlaAsnPheThrLeuProAspSerGluPheLeuLysIleP
5710 5720 5730 5740 5750 5760
TTAAGCCGGAGCGGCCTTCCTGCCCGAGTGGTGGGCATTAAATGCAGACTTGTCTCCAC
heLysProGluAlaAlaPheLeuProGluTrpValGlyLeuAsnAlaAspLeuSerProL
5770 5780 5790 5800 5810 5820
TCTGGACATTGGCTAAGCCTTGAGAGCCAGGGAGACTTCTGAAAGTAGCCTGATCTTTCT
euTrpThrLeuAlaLysProEnd
5830 5840 5850 5860 5870 5880
AGAGCCAGCAGTACGTGGCTTCAGAGGCCCTGGCATCTTCTGGAGAAGCTTGTGGTGTTC
5890 5900 5910 5920 5930 5940
TGAAGCAAATGGGTGCCCGTATCCAGAGTGATTCTAGTTGGGAGAGTTGGAGAGAAGGGG
5950 5960 5970 5980 5990 6000
GACGTTTCTGGAACTGTCTGAATATTCTAGAACTAGCAAAACATCTTTCTGATGGCTG
6010 6020 6030 6040 6050 6060
GCAGGCAGTTCTAGAAAGCCACAGTGCCCACTGCTCTTCCCAGCCCCATATCTACAGTACT
6070 6080 6090 6100 6110 6120
TCCAGATGGCTGCCCCCAGGAATGGGAACTCTCCCTCTGTGTCTACTCTAGAAGAGGGGT
6130 6140 6150 6160 6170 6180
TACTTCTCCCCCTGGGTCTCCAAAGACTGAAGGAGCATATGATTGCTCCAGAGCAAGCAT

FIG. 3J

6190 6200 6210 6220 6230 6240
TCACCAAGTCCCCCTTCTGTGTTTCTGGAGTGATTCTAGAGGGAGACTTGTCTTAGAGAGG

6250 6260 6270 6280 6290 6300
ACCAGGTTTGATGCCCTGTGAAGAACCCCTGCAGGGCCCTTATGGACAGGATGGGTTCTTGG

6310 6320 6330 6340 6350 6360
AAATCCAGATAACTAAGGTGAAGAACTTTTTAGTTTTTTTTTTTTTTTTGGAGACAG

6370 6380 6390 6400 6410 6420
GGTCTCGCTCTGTTGCCCCAGGCTGGAGTGCACTGGCGTGATCTTGGCTCACTGCAACTTC

6430 6440 6450 6460 6470 6480
CGCCTCCTGTGTTCAAGCGATTCTCCTGTCTCAGCCCTCCTAGTAGATGGGACTACAGGC

6490 6500 6510 6520 6530 6540
ACAGGCCATTATGCCCTGGCTAATTTTGTATTTTAGTAGAGACAGGGTTTCACCATGTT

6550 6560 6570 6580 6590 6600
GGCCGGGATGGTCTCGATCTCCTGACCTTGTCATCCACCTGTCTTGGCCTCCCAAAGTGC

6610 6620 6630 6640 6650 6660
TGGGATTACTGGCATGAGCCACTGTGCCCCAGCCCCGGATATTTTTTTTAAATTATTTATT

6670 6680 6690 6700 6710 6720
ATTTATTTATTATTGAGACGGAGTCTTGCTCTGTAGCCCCAGGCCAGAGTGCAGTGGCGC

6730 6740 6750 6760 6770 6780
GATCTCAGCTCACTGCAAGCTCTGCTCCCGGGTTTCATGCCATTCTGCCTCAGCCTCCTG

6790 6800 6810 6820 6830 6840
AGTAGCTGGGACTACAGGGCCCCGCCACCAGCCCCGGCTAATTTTTTTTGTATTTTAGT

FIG. 3K

6850 6860 6870 6880 6890 6900
AGAGACGGGTTTCATCGTTTAAACCAGGATGGTCTCGATCTCCTGACCTCGTGATCTGC
6910 6920 6930 6940 6950 6960
CCACCTCGGCCCTCCACAGTGTCTGGGATTACCGGCGTGAGCCACCATGCCTGGCCCGGAT
6970 6980 6990 7000 7010 7020
AATTTTAAATTTTGTAGAGACGAGGTCTTGTGATATTGCCCAGGCTGTTCTTCAAC
7030 7040 7050 7060 7070 7080
TCCTGGGCTCAAGCAGTCTCTCCACCTTGGCCTCCAGAAATGCTGGGTTTATAGATGTGA
7090 7100 7110 7120 7130 7140
GCCAGCACACCGGGCCAAAGTGAAGAACTAATGAATGTGCAACCTAATTGTAGCATCTAA
7150 7160 7170 7180 7190 7200
TGAATGTTCCACCATTTGCTGGAAAAATTGAGATGGAAAAACAACCATCTCTAGTTGGCCA
7210 7220 7230 7240 7250 7260
GCGTCTTGCTCTGTTACAGTCTCTGAAAAAGCTGGGGTAGTTGGTGAGCAGAGCGGGAC
7270 7280 7290 7300 7310 7320
TCTGTCCAAACAAGCCCCACAGCCCTCAAAGACTTTTTTTTGTGTTTGTGAGCAGACAG
7330 7340 7350 7360 7370 7380
GCTAAATGTGAACGTGGGTGAGGGATCACTGCCAAAAATGGTACAGCTTCTGGAGCAGA
7390 7400 7410 7420 7430 7440
ACTTTCCAGGGATCCAGGGACACTTTTTTTTAAAGCTCATAACTGCAAGAGCTCCATA
7450 7460 7470 7480 7490 7500
TATTGGGTGTGAGTTTCAAGTTGCCCTCTCACAATGAAGGAAGTTGGTCTTTGTCTGCAGGT

FIG. 3L

FIG. 3M

7510 7520 7530 7540 7550 7560
GGGCTGCTGAGGGTCTGGGATCTGTTTTCTGTGAAGTGTGCAGGTATAAACACACACCCCTCTG
7570 7580 7590 7600 7610 7620
TGCTTGTGACAAACTGGCAGGTACCGTGCTCATTTGCTAACCACTGTCTGTCCCTGAACCTC
7630 7640 7650 7660 7670 7680
CCAGAACCACTACATCTGGCTTTGGCAGGTCTGAGATAAAACGATCTAAAGTAGGCAG
7690 7700 7710 7720 7730 7740
ACCCTGAGACCCAGCCTCAGATCCAGGACGAGCAGGCTGTGCCAAGGTGGACGGGGT
7750 7760 7770 7780 7790 7800
TGTCGAGATCTCAGGAGCCCCCTTGCTGTTTTTTGGAGGGTGAAAGAAACCTTAAACA
7810 7820 7830 7840 7850 7860
TAGTCAGCTCTGATCACATCCCCCTGTCTACTCATCCAGACCCCATGCCCTGTAGGCTTATC
7870 7880 7890 7900 7910 7920
AGGGAGTTACAGTTACAATTGTTACAGTACTGTTCCCAACTCAGCTGCCACGGGTGAGAG
7930 7940 7950 7960 7970 7980
AGCAGGAGGTATGAATTAAAGTCTACAGCACTAACCCGTGTCTCTGTAGCTTTTTTTGGA
7990 8000 8010 8020 8030 8040
GCCAGAGCCACTGTGTATGTGTGTGGGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
8050 8060 8070 8080 8090 8100
AAGAGAGTGGAGGAAAAGGTGGGGTACTTCTGAAGACTTTTATTTTTTTTTTAATAATTT
8110 8120 8130 8140 8150 8160
ATTTTTTTCAGAGATCGAGTCTTGCTCTGTGGCCAGGCTGGAGTGCAGTAGTGTGATC

FIG. 3N

8170
TCGGCCCACTGCAA

FIG. 3N

FIG. 4A

10	20	30	40	50	60
* CTGCA GAGAG CGCCA CCCGG AAGCC ACTTT TATAG AAGCT TTTAC ACACA ATGCT TGATT					
70	80	90	100	110	120
* TTTT TTTT TTTT CGAGA CGGAG TCTCG CTTTG TCGCC CAGGC TGGAG TGCAG TGGCG					
130	140	150	160	170	180
* CGATC TGGGC TCACT GCAAG CTCCG CCTCC TGGGT TGACG CCATT CTCCT GCCTC AGCTT					
190	200	210	220	230	240
* CCCGA GTAGC TGGGA CTACA GCGC CCGCC ACCAA GCCTG GCTAA TTTT TTTTA TTTT					
250	260	270	280	290	300
* AGTGG AGACA GAGTT TCACC GTGTT AGCCA GGATG GTCTC GATCT CCTGA CCTCG GGATC					
310	320	330	340	350	360
* CGCCC GCCTC GGCCT CCCAA AGTGC TGGGA GTATA GCGGT GAGCC ACCGC GCCTG GCCTA					
370	380	390	400	410	420
* TACTT GATT TTAAT GAAAA CATT CTTAA TTCAAT ATGGC TAACG CAAAT TTATT TTCTG					
430	440	450	460	470	480
* TAGGC ATAAC ATCAA AAACA CCTGG CAGGA CTGCC CCATT CCCAG CACTG TCTAG TTCTC					

FIG. 4A

"Sheet" 3860

490	*	500	510	520	530	540
CCCTA	GTATC	AGTGG	GACTC	CACTG	ATGCA	CAGCT
						GTGAT
						CTACT
						AAAAC
						TTCTC
						TCAAA
550	*	560	570	580	590	600
ACTTT	CTCCT	CTCCT	TAGGT	CAGCA	GCCCC	GCCTC
						TGATC
						TATTT
						GGAAA
						TCCCC
						TGAAT
610	*	620	630	640	650	660
AAAAA	TTGAA	TATCA	TAAAC	CAAAAG	CGAAC	ACCCA
						GAAAT
						TCAAA
						TTCAA
						CCCCG
						TAGTA
670	*	680	690	700	710	720
AAAAA	TTTCT	CAAGT	GACTG	TAGAC	GTAGA	TGTCT
						CCAGT
						GTGCG
						CTAAT
						AAGGT
						AGAAG
730	*	740	750	760	770	780
AGGCC	AGTGC	GATAC	TGTCT	TTACA	CCCTT	AACCT
						GGGTG
						CTAGA
						ATATT
						TATCT
						TCGTC
790	*	800	810	820	830	840
ATCAT	TTTAT	CATCC	AAACT	ATTTT	GCATA	ACTTT
						CATGG
						GTGCA
						GAAAA
						TGTTT
						TTTAA
850	*	860	870	880	890	900
GTGCT	TGGTA	AAATT	AATAG	TGATA	TTCAT	TCATT
						CATCT
						CACTG
						AACAG
						GCAAT
						AAATT
910	*	920	930	940	950	960
CCTTG	ACGAC	AAGGG	CCTTG	GGGGG	GGCCA	CATCT
						TCATC
						TTTGG
						TTTAT
						GAGTC
						CTGTG

FIG. 4B

970	980	990	1000	1010	1020
* TGGTA	* CAAGC	* AATAC	* TACTA	* TGAGC	* TGAGC
CGTCT	CAAGC	AATAC	TACTA	TGAGC	TGAGC
1030	1040	1050	1060	1070	1080
* AAAGA	* ACATG	* TTTTG	* AAACA	* TTTTG	* TTTTG
AAAGG	AAAGA	ACATG	TTTTG	TTTTC	TTTTC
1090	1100	1110	1120	1130	1140
* GGCAA	* AGGAA	* ATGTT	* CTCAC	* AAAC	* AAAC
TGGCA	GGCAA	AGGAA	CTCAC	AAAC	AAAC
1150	1160	1170	1180	1190	1200
* GAGAC	* TCTGA	* AGGCC	* AGGCC	* GCTGC	* GCTGC
ATGCA	GAGAC	TCTGA	AGGCC	GCTGC	GCTGC
1210	1220	1230	1240	1250	1260
* ACGAG	* ATCCT	* GGCCA	* CGGAT	* GCGGT	* GCGGT
GGGCC	ACGAG	ATCCT	GGCCA	GCGGT	GCGGT
1270	1280	1290	1300	1310	1320
* GGACT	* CCTTC	* CCTCC	* CTCAA	* TCCCT	* TCCCT
CCTCT	GGACT	CCTTC	CCTCC	CTCAA	TCCCT
1330	1340	1350	1360	1370	1380
* CAACG	* GCAGG	* AAGCC	* GACGC	* TATCC	* TATCC
AGGCC	CAACG	GCAGG	AAGCC	GACGC	TATCC
1390	1400	1410	1420	1430	1440
* TCTAG	* GGCCT	* GCTCC	* TGCCT	* TGCCT	* TGCCT
TCTGT	TCTAG	GGCCT	GCTCC	TGCCT	TGCCT

FIG. 4C

FIG. 4D

1450	1460	1470	1480	1490	1500
* CTTCC CAGGG ATGAA CCGGG CCTTC CCTCT * GGAAG GCGAG GGTTC GGGCC ACAGT GAGCG					
1510	1520	1530	1540	1550	1560
* AGGGC CAGGG CGGTG GCGGC GCGCA GAGGG AAACC GGATC AGTTG AGAGA GAATC AAGAG					
1570	1580	1590	1600	1610	1620
* TAGCG GATGA GCGGC TTGTG GGGCG CCGCC CGGAA GCCCT CCGGC CCGCT CTGGG AGAAG					
1630	1640	1650	1660	1670	1680
* GAGTG GCGCG AGGCG CCGCA GGAGG CTCCC CCGGC CTGGT CCGGC CCGCT GGGCC CCGGG					
1690	1700	1710	1720	1730	1740
* CGCAG TGGAA GAAAG GGACG GCGCG TGCCC GGTG GCGGT CCTGG CCAGC TCACC TTGCC					
1750	1760	1770	1780	1790	1800
* CTGGC GGCTC GCCCC GCCCG GCACT TGGGA GGAGC AGGGC CCGCG GCCTT TGCAT					
1810	1820	1830	1840	1850	1860
* TCTGG GACCG CCCCC TTCCA TTCCC GGGCC AGCGG CGAGC GGCAG GCTGG AGCCG					
1870	1880	1890	1900	1910	1920
* CAGCT ACAGC ATGAG AGCCG GTGCC GCTCC TCCAC GCCTG CCGAC GCGTG GCGAG CGGAG					

FIG. 4D

FIG. 4E

1930	1940	1950	1960	1970
* GCAGC GCTGC CTGTT CGCGC C	* ATG GGG GCA CCG TGG GGC TCG CCG ACC GCG GCG	* Met Gly Ala Pro Trp Gly Ser Pro Thr Ala Ala	* Met Gly Ala Pro Trp Gly Ser Pro Thr Ala Ala	* Met Gly Ala Pro Trp Gly Ser Pro Thr Ala Ala
1980	1990	2000	2010	2020
* GCG GGC GGG CCG CGC GGC TGG CGC GGC GGC CTG CCA TGG ACC GTC TGT	* Ala Gly Gly Arg Arg Gly Trp Arg Arg Gly Arg Gly Leu Pro Trp Thr Val Cys	* GCG GGC GGG CCG CGC GGC TGG CGC GGC GGC CTG CCA TGG ACC GTC TGT	* Ala Gly Gly Arg Arg Gly Trp Arg Arg Gly Arg Gly Leu Pro Trp Thr Val Cys	* GCG GGC GGG CCG CGC GGC TGG CGC GGC GGC CTG CCA TGG ACC GTC TGT
2030	2040	2050	2060	2070
* GTG CTG GCG GCC GCG GGC TGT ACG TGT ACG GCG CTG ATC ACC TAC GCT TGC TGG	* Val Leu Ala Ala Ala Gly Leu Thr Cys Thr Ala Leu Ile Thr Tyr Ala Cys Trp	* GTG CTG GCG GCC GCG GGC TGT ACG TGT ACG GCG CTG ATC ACC TAC GCT TGC TGG	* Val Leu Ala Ala Ala Gly Leu Thr Cys Thr Ala Leu Ile Thr Tyr Ala Cys Trp	* GTG CTG GCG GCC GCG GGC TGT ACG TGT ACG GCG CTG ATC ACC TAC GCT TGC TGG
2090	2100	2110	2120	2130
* GGG CAG CTG CCG CCG CTG CCC TGG GCG TCG CCA ACC CCG TCG CGA CCG GTG GGC	* Gly Gln Leu Pro Pro Leu Trp Ala Ser Pro Thr Pro Ser Arg Pro Val Gly	* GGG CAG CTG CCG CCG CTG CCC TGG GCG TCG CCA ACC CCG TCG CGA CCG GTG GGC	* Gly Gln Leu Pro Pro Leu Trp Ala Ser Pro Thr Pro Ser Arg Pro Val Gly	* GGG CAG CTG CCG CCG CTG CCC TGG GCG TCG CCA ACC CCG TCG CGA CCG GTG GGC
2140	2150	2160	2170	2180
* CTG CTG CTG TGG TGG GAG GAG CCC TTC GGG GGC CGC GAT AGC GCC CCG AGG CCG CCC	* Val Leu Leu Trp Trp Glu Pro Phe Gly Gly Arg Asp Ser Ala Pro Arg Pro Pro	* CTG CTG CTG TGG TGG GAG GAG CCC TTC GGG GGC CGC GAT AGC GCC CCG AGG CCG CCC	* Val Leu Leu Trp Trp Glu Pro Phe Gly Gly Arg Asp Ser Ala Pro Arg Pro Pro	* CTG CTG CTG TGG TGG GAG GAG CCC TTC GGG GGC CGC GAT AGC GCC CCG AGG CCG CCC
2200	2210	2220	2230	2240
* CCT GAC TGC CCG CTG CGC TTC AAC ATC AGC GGC TGC CGC CTG CTC ACC GAC CGC	* Pro Asp Cys Pro Leu Arg Arg Phe Asn Ile Ser Gly Cys Arg Leu Thr Asp Arg	* CCT GAC TGC CCG CTG CGC TTC AAC ATC AGC GGC TGC CGC CTG CTC ACC GAC CGC	* Pro Asp Cys Pro Leu Arg Arg Phe Asn Ile Ser Gly Cys Arg Leu Thr Asp Arg	* CCT GAC TGC CCG CTG CGC TTC AAC ATC AGC GGC TGC CGC CTG CTC ACC GAC CGC
2250	2260	2270	2280	2290
* GCG TCC TAC GGA GAG GCT CAG GCC GTG CTT TTC CAC CAC CGC GAC CTC GTG AAG	* Ala Ser Tyr Gly Glu Ala Ala Val Leu Phe His Arg Asp Leu Val Lys	* GCG TCC TAC GGA GAG GCT CAG GCC GTG CTT TTC CAC CAC CGC GAC CTC GTG AAG	* Ala Ser Tyr Gly Glu Ala Ala Val Leu Phe His Arg Asp Leu Val Lys	* GCG TCC TAC GGA GAG GCT CAG GCC GTG CTT TTC CAC CAC CGC GAC CTC GTG AAG

FIG. 4E

FIG. 4F

FIG. 4F

2300 *	2310 *	2320 *	2330 *	2340 *	2350 *
GGG CCC CCC GAC TGG CCC CCG CCC TGG GGC ATC CAG GCG CAC ACT GCC GAG GAG					
Gly Pro Pro Asp Trp Trp Pro Pro Trp Gly Ile Gln Ala His Thr Ala Glu Glu					
2360 *	2370 *	2380 *	2390 *	2400 *	
GTG GAT CTG CGC GTG TTG GAC TAC GAG GAG GCA GCG GCG GCA GAA GCC CTG					
Val Asp Leu Arg Val Leu Asp Tyr Glu Glu Ala Ala Ala Glu Ala Leu					
2410 *	2420 *	2430 *	2440 *	2450 *	2460 *
GCG ACC TCC AGC CCC AGG CCC CCG GGC CAG CGC TGG GTT TGG ATG AAC TTC GAG					
Ala Thr Ser Ser Pro Arg Pro Pro Gly Gln Arg Trp Val Trp Met Asn Phe Gln					
2470 *	2480 *	2490 *	2500 *	2510 *	
TCG CCC TCG CAC TCC CCG GGC CTG CGA AGC CTG GCA AGT AAC CTC TTC AAC TGG					
Ser Pro Ser His ser Pro Gly Leu Arg Ser Leu Ala Ser Asn Leu Phe Asn Trp					
2520 *	2530 *	2540 *	2550 *	2560 *	
ACG CTC TCC TAC CCG GCG GAC TCG GAC GTC TTT GTG CCT TAT GGC TAC CTC TAC					
Thr Leu Ser Tyr Arg Ala Asp Ser Asp Val Phe Val Pro Tyr Gly Tyr Leu Tyr					
2570 *	2580 *	2590 *	2600 *	2610 *	2620 *
CCC AGA AGC CAC CCC GGC GAC CCC TCA GGC CTG GCC CCG CCA CTG TCC AGG					
Pro Arg Ser His Pro Gly Asp Pro Pro Ser Gly Leu Ala Pro Pro Leu Ser Arg					
2630 *	2640 *	2650 *	2660 *	2670 *	
AAA CAG GGC CTG GTG GCA TGG GTG GTG AGC CAC TGG GAC GAG CGC CAG GCC CGG					
Lys Gln Gly Leu Val Ala Trp Val Val Ser His Trp Asp Glu Arg Gln Ala Arg					

2680	2690	2700	2710	2720	2730
* GTC CGC TAC TAC CAC CAA CAT GTG ACC GTG GAC GTG TTC GGC CGG	* Val Arg Tyr Tyr His Gln Leu Ser Gln His Val Thr Val Asp Val Phe Gly Arg				
2740	2750	2760	2770	2780	
* CGC GGC CCC GGG CAG CCG GTG CCC GAA ATT GGG CTC CTG CAC ACA GTG GCC CGC	* Gly Gly Pro Gly Gln Pro Val Pro Gln Ile Gly Leu Leu His Thr Val Ala Arg				
2790	2800	2810	2820	2830	
* TAC AAG TTC TAC TAC GCT TTC GAG AAC TCG CAG CAC CTG GAT TAT ATC ACC GAG	* Tyr Lys Phe Tyr Leu Ala Phe Gln Asn Ser Gln His Leu Asp Tyr Ile Thr Glu				
2840	2850	2860	2870	2880	2890
* AAG CTC TGG CGC AAC GCG TTG CTC GCT GGG GCG GTG CCG GTG GTG CTG GGC CCA	* Lys Leu Trp Arg Asn Ala Leu Leu Ala Gly Ala Val Pro Val Val Leu Gly Pro				
2900	2910	2920	2930	2940	
* GAC CGT GCC AAC TAC GAG CCG TTT GTG CCC CGC GGC GCC TTC ATC CAC GTG GAC	* Asp Arg Ala Asn Tyr Glu Arg Phe Val Pro Arg Gly Ala Phe Ile His Val Asp				
2950	2960	2970	2980	2990	3000
* GAC TTC CCA AGT GCC TCC TCC CTG GCC TCG TAC CTG CTT TTC CTC GAC CGC AAC	* Asp Phe Pro Ser Ala Ser Ser Ser Leu Ala Ser Tyr Tyr Leu Leu Phe Leu Asp Arg Asn				
3010	3020	3030	3040	3050	
* CCC GCG GTC TAT CGC CGC TAC TTC CAC TGG CGC CGG AGC TAC GCT GTC CAC ATC	* Pro Ala Val Tyr Arg Arg Tyr Phe His Trp Arg Arg Ser Tyr Ala Val His Ile				

FIG. 46

3060	3070	3080	3090	3100
* ACC TCC TTC TGG GAC GAG CCT TGG TGC CGG GTG TGC CAG GCT GTA CAG AGG GCT				*
Thr Ser Phe Trp Asp Glu Pro Trp Cys Arg Val Cys Gln Ala Val Gln Arg Ala				
3110	3120	3130	3140	3150
* GGG GAC CGG CCC AAG AGC ATA CGG AAC TTG GCC AGC TGG TTC GAG CGG TGA A		*	*	*
Gly Asp Arg Pro Lys Ser Ile Arg Asn Leu Ala Ser Trp Phe Glu Arg ***				
3170	3180	3190	3200	3210
* GCCGC GCTCC CCTGG AAGCG ACCCA GGGGA GGGCA AGTTG TCAGC TTTT GATCC TCTAC		*	*	*
3230	3240	3250	3260	3270
* TGTGC ATCTC CTTGA CGGCC GCATC ATGGG AGTAA GTTCT TCAAA CACCC ATTTT TGCTC		*	*	*
3290	3300	3310	3320	3330
* TATGG GAAAA AAACG ATTTA CCAAT TAATA TTACT CAGCA CAGAG ATGGG GGCCC GGTTT		*	*	*
3350	3360	3370	3380	3390
* CCATA TTTT TGCAC AGCTA GCAAT TGGGC TCCCT TTGCT GCTGA TGGGC ATCAT TGTTT		*	*	*
3410	3420	3430	3440	3450
* AGGGG TGAAG GAGGG GTTTC TTCCT CACCT TGTA CCAGT GCAGA AATGA AATAG CTTAG		*	*	*
3470	3480	3490	3500	3510
* CGGCA AGAAG CCGTT GAGGC GGTTT CCTGA ATTTC CCCAT CTGCC ACAGG CCATA TTTGT		*	*	*
				3520
				*

3530 * 3540 * 3550 * 3560 * 3570 * 3580 *
GGCCC GTGCA GCTTC CAAAT CTCAT ACACA ACTGT TCCCG ATTCA CGTTT TTCTG GACCA
3590 * 3600 * 3610 * 3620 * 3630 * 3640 *
AGGTG AAGCA AATTT GTGGT TGTAG AAGGA GCCTT GTTGG TGGAG AGTGG AAGGA CTGTG
GCTGC AG

FIG. 4I

DOCKET SHEET

pFT-3 DNA	ATGGGGGCACCGTGGGGCTCGCCGACGGCGGGCGGGCGGGCGGGCGGGTG	
pFT-3 AA	1 M G A P W G S P T A A A G G R R G W18	
Lewis AA	1 M D . P L G . . . A A K P Q W P W13	
pFT-3 DNA	GGCGGAGGCGGGGGCTGCCATGGACCGTCTGTGTGGCGGCC-----	
pFT-3 AA	19 R R G R G L P W T V C V L A A . . 33	
Lewis AA	14 R R C . L A A L L 22	
pFT-3 DNA	--GCCCGGCTTGACGTGTACGGCGGATCACCTAC-----GCT	
pFT-3 AA	34. A G L T C T A L I T Y . . A 45	
Lewis AA	23F Q L L V A V C F F S Y L R V 36	
pFT-3 DNA	TGCTGGGGGCAGCTGCCCGCGCTGCCCTGGCG-----TCGCCA-----	
pFT-3 AA	46 C W G Q L P P L P W A . . . S P . 58	
Lewis AA	37 S R D D A T G S P R A P S G S S R Q54	
pFT-3 DNA	-----ACCCCGTCGCGACCG---GTGGGCGTGTGTGTGG---TGGGAGC	
pFT-3 AA	59 . . T P S R P . V G V L L W . W E 71	
Lewis AA	55 D T T P T R P T L L I L L W T W . 70	
pFT-3 DNA	CCTTCGGGGCGCGATAGCGCCCGAGGCGGCCCTGACTGC	
pFT-3 AA	72P F G G R D S A P R P P P D C 86	
Lewis AA	71P F H I P V A L S R C . . S 82	

FIG. 5A

pFT-3 DNA	CCGCTGCGCTTCAACATCAGCGGCTGCCGCTGCTCACCACCGCGCGTCCTA	
pFT-3 AA	87 P L R F N I S G C R L L T D R A S Y104	
Lewis AA	83 E M V P G T A D C H I T A D R K V Y100	
pFT-3 DNA	CGGAGAGGCTCAGCGCGTGTCTTTCCACCACCGCGACCTCGTGAAGGGCCCC	
pFT-3 AA	105 G E A Q A V L F H H R D L V K G P 121	
Lewis AA	101 P Q A D T V I V H H W D I M S N P 117	
pFT-3 DNA	CCGACTGGCCCCCGCCCTGGGGCATCCAGGCGCACACTGCCGAG	
pFT-3 AA	122P D W P P P W G I Q A H T A E 136	
Lewis AA	118K S R L P P 123	
pFT-3 DNA	GAGGTGGATCTGCGCGTGTGGACTACGAGGAGCGCGCGGCGGAGAGC	
pFT-3 AA	137 E V D L R V L D Y E E A A A A E A154	
Lewis AA	124 124	
pFT-3 DNA	CCTGGCGACCTCCAGCCCCAGGCCCGCGGCGCAGCGCTGGGTTGGATGAAC	
pFT-3 AA	155 L A T S S P R P P P G Q R W V W M N 171	
Lewis AA	124 136	
pFT-3 DNA	TCGAGTCGCCCTCGCACTCCCGGGGCTGCGAAGCCTGGCAAGT	
pFT-3 AA	172F E S P S H S P G L R S L A S 186	
Lewis AA	137L E P P P N C Q H L E A L D . 150	

FIG. 5B

pFT-3 DNA	AACCTCTTCAACTGGACGCTCTCTACCGGGGAGCTCGGACGTCTTTGTGCC	
pFT-3 AA	187 N L F N W T L S Y R A D S D V F V P204	
Lewis AA	151 R Y F N L T M S Y R S D S D I F T P168	
pFT-3 DNA	TTATGGCTACCTCTACCCAGAAAGC---CACCCCGGACCCCGCCCTCAGGCC	
pFT-3 AA	205 Y G Y L Y P R S . H P G D P P S G 220	
Lewis AA	169 Y G W L E P W S G Q P A H P P . 183	
pFT-3 DNA	TGGCCCCGCACTGTCCAGAAACAGGGCTGGTGGCATGGGTG	
pFT-3 AA	221L A P P L S R K Q G L V A W V 235	
Lewis AA	184L N . L S A K T E L V A W A 196	
pFT-3 DNA	GTGAGCCACTGGGACGAGCGCCAGGCCGGGTCCGCTACTACCAACTGAG	
pFT-3 AA	236 V S H W D E R Q A R V R Y Y H Q L S253	
Lewis AA	197 V S N W K P D S A R V R Y Y Q S L Q214	
pFT-3 DNA	CCAACATGTGACCGTGGACGTGTTCCGGCCGGGCGGCGGCGGCGGTGC	
pFT-3 AA	254 Q H V T V D V F G R G G P G Q P V 270	
Lewis AA	215 A H L K V D V Y G R S . H K P L 229	
pFT-3 DNA	CCGAAATTGGGCTCTGCACACAGTGGCCCGCTACAAGTTCTAC	
pFT-3 AA	271P E I G L L H T V A R Y K F Y 285	
Lewis AA	230P K G T M M E T L S R Y K F Y 244	

FIG. 5C

pFT-3 DNA	CTGGCTTTCGAGAACTCGCAGCACCTGGATTATATACCGAGAAAGCTCTGGCG
pFT-3 AA	286 L A F E N S Q H L D Y I T E K L W R303
Lewis AA	245 L A F E N S L H P D Y I T E K L W R262
pFT-3 DNA	CAACGCGTTGCTCGCTGGGGCGGTGCCGTGTGTGGGCCCGACCGTGCCCA
pFT-3 AA	304 N A L L A G A V P V V L G P D R A 320
Lewis AA	263 N A L E A W A V P V L G P S R S 279
pFT-3 DNA	ACTACGAGCGCTTGTGCCCGCGCGCTTCATCCACGTGGAC
pFT-3 AA	321N Y E R F V P R G A F I H V D 335
Lewis AA	280N Y E R F L P P D A F I H V D 294
pFT-3 DNA	GACTTCCCAAGTGCCTCCTCCCTGGCCTCGTACCTGCTTTCTCGACCGCAA
pFT-3 AA	336 D F P S A S S L A S Y L L F L D R N353
Lewis AA	295 D F Q S P K D L A R Y L Q E L D K D312
pFT-3 DNA	CCCCGGGTCTATCGCCGCTACTTCCACTGGCGC-----CGGA
pFT-3 AA	354 P A V Y R R Y F H W R . . . R 365
Lewis AA	313 H A R Y L S Y F R W R E T L R P R 329
pFT-3 DNA	GCTACGCTGTCCACATCACCTCCTTC---TGGGACGAGCCTTGG
pFT-3 AA	366S Y A V H I T S F . W D E P W 379
Lewis AA	330S F S W A L D . . F 337

FIG.5D

pFT-3 DNA	TGCCGGGTGTGCCAGGCTGTACAGAGGGCTGGGGACCGGCCCAAGAGCATACG	
pFT-3 AA	380 C R V C Q A V Q R A G D R P K S I R397	
Lewis AA	338 C K A C W K L Q Q E S . R Y Q T V R354	
pFT-3 DNA	GAACTTGGCCAGCTGGTTCGAGCGGTGA	
pFT-3 AA	398 N L A S W F E R 405	
Lewis AA	355 S I A A W F T . 361	

FIG. 5E

-60 TGGGTGATCTTCCCTTAATGACCCCTCACTCCTCTCTCCTCTCTTCCCAGCTACTCTGACCC

61 L F Q L L V A V C F F S Y L R V S R D D
CTGTTTCAGCTGCTGGTGGCTGTGTGTTTCTTCTCTACCTGCGTGTGTCCCGAGACGAT
CTATTTTCAGCTGCTGGTGGCTGTGTGTTTCTTCTCTACCTGCGTGTGTCCCGAGACGAT

181 G S R C Q D S M A T P A H P T L L I L L
GGTCCCGCTGCCAGGACAGCATGGGACCCCTGCCCCACCCCTACTGATCCTGCTG
GGTCTCCCGACGAGACAC-----ACTCCACCCGCCACCCCTCCTGATCCTGCTA
S R S R T R

FIG. 6A

W T W P F N T P V A L P R C S E M V P G
241 TGGACGTGGCCCTTTAACAACACCCGTGGCTCTGCCCGCTGCTCAGAGATGGTCCCGGC
TGGACATGGCCCTTCCACATCCCTGTGGCTCTGTCCCGCTGTTTCAGAGATGGTCCCGGC
H I S

A A D C N I T A D S S V Y P Q A D A V I
301 GGGCCGACTGCAACATCACTGCCGACTCCAGTGTTGTTACCCACAGGACGCGGTCTCATC
ACAGCCGACTGCCACATCACTGCCGACCGCAAGTGTTACCCACAGGACGACGCTCATC
T H R K T

V H H W D I M Y N P S A N L P P T R P
361 GTGCACCACTGGGATATCATGTCAACCCCAAGTGCCAACTCCCGCCCCCAGGCGG
GTGCACCACTGGGATATCATGTCAACCCCAAGTGCCAACTCCCGCCCCCAGGCGG
S K S R S P

Q G Q R W I W F S M E S P S N C R H L E
421 CAGGGCAGCGCTGGATCTGGTTTCAGCATGGAGTCCCCCAGCAACTGCCGACCTGGAA
CAGGGCAGCGCTGGATCTGGTTCAACTTGGAGCCACCCCTAACTGCCAGCACCTGGAA
N L P P Q

A L D G Y F N L T M S Y R S D S D I F T
481 GCCCTGGACGGATACTTCAATCTCACCATGTCTACCGCAGCGACTCCGACATCTTCACG
GCCCTGGACAGATACTTCAATCTCACCATGTCTACCGCAGCGACTCCGACATCTTCACG
R

P Y G W L E P W S G Q P A H P P L N L S
541 CCCTACGGCTGGAGCCGTGGTCCGGCCAGCCTGCCACCCACCGCTCAACCTCTCG
CCCTACGGCTGGAGCCGTGGTCCGGCCAGCCTGCCACCCACCGCTCAACCTCTCG

FIG. 6B

601 A K T E L V A W A V S N W K P D S A R V
GCCAAGACOGAGCTGGTGGCCCTGGCGGTGTCCAAGTGAAGCCGGACTCGGCCAGGGTG
GCCAAGACOGAGCTGGTGGCCCTGGCGGTGTCCAAGTGAAGCCGGACTCGGCCAGGGTG

661 R Y Y Q S L Q A H L K V D V Y G R S H K
CGTACTACGAGCCTGCGAGGCTCATCTCAAGTGGACGTGTACGGACGCTCCACAAG
CGTACTACGAGCCTGCGAGGCTCATCTCAAGTGGACGTGTACGGACGCTCCACAAG

721 P L P K G T M M E T L S R Y K F Y L A F
CCCCTGCCCAAGGGACCATGATGGAGACGCTGTCCCGGTACAAGTTCATCTGGCCCTTC
CCCCTGCCCAAGGGACCATGATGGAGACGCTGTCCCGGTACAAGTTCATCTGGCCCTTC

781 E N S L H P D Y I T E K L W R N A L E A
GAGAACTCCTTGACCCCGACTACATCACCAGAAAGCTGTGGAGGAACGCCCTGGAGGCC
GAGAACTCCTTGACCCCGACTACATCACCAGAAAGCTGTGGAGGAACGCCCTGGAGGCC

841 W A V P V V L G P S R S N Y E R F L P P
TGGCCGTGCCCGTGGTGTGGTGGCCCGCCAGCAGAACTACGAGAGGTTCTTCCGCCCC
TGGCCGTGCCCGTGGTGTGGTGGCCCGCCAGCAGAACTACGAGAGGTTCTTCCGCCCC

901 D A F I H V D D F Q S P K D L A R Y L Q
GAGCCCTTCATCCACGTGGATGACTTCCAGAGCCCCAAGGACCTGGCCCGGTACCTGCAG
GAGCCCTTCATCCACGTGGACGACTTCCAGAGCCCCAAGGACCTGGCCCGGTACCTGCAG

961 E L D K D H A R Y L S Y F R W R E T L R
GAGCTGGACAAGGACCAAGCCCGTACCTGAGTACTTTCGCTGGCGGAGACGCTGCGG
GAGCTGGACAAGGACCAAGCCCGTACCTGAGTACTTTCGCTGGCGGAGACGCTGCGG

FIG. 6C

P R S F S W A L A F C K A C W K L Q Q E
1021 CCTCGCTCCTTCAGCTGGGCACTGGCTTTCTGCAAGGCCTGCTGGAAGCTGCAGCAGGAA
CCTCGCTCCTTCAGCTGGGCACTGGATTTCTGCAAGGCCTGCTGGAAGCTGCAGCAGGAA
D

S R Y Q T V R S I A A W F T U
1081 TCCAGGTACACAGACGGTGCGCAGCATAGCGGCTTGGTTACCTGAGAGGCCGGCATGGGG
TCCAGGTACACAGACGGTGCGCAGCATAGCGGCTTGGTTACCTGA

1141 CCTGGGCTGCCAGGGACCTCACTTTCCAGGGCCTCACCTACCTAGGTC // TCTAGA

FIG. 6D

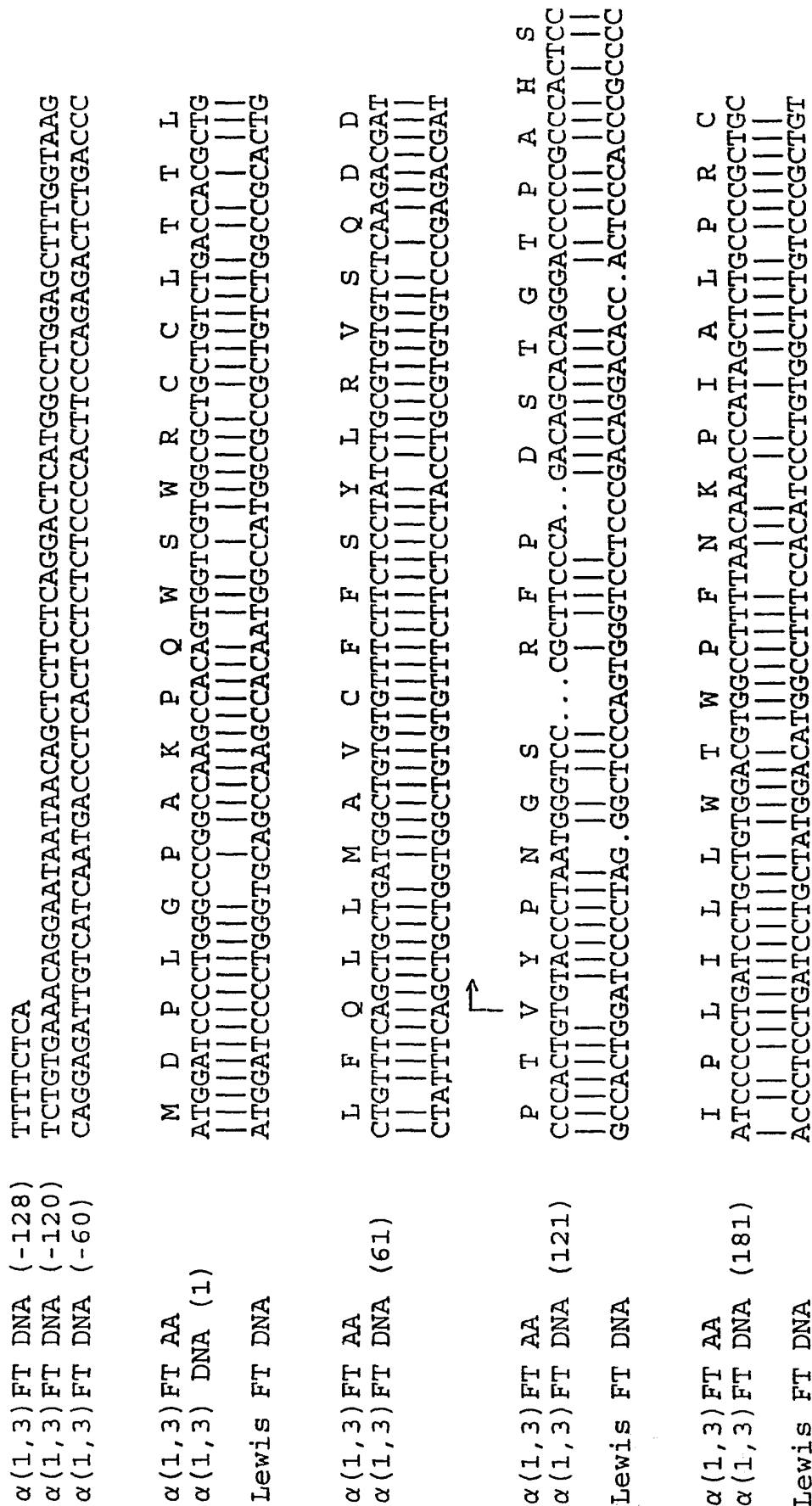


FIG. 7A

S E M V P G T A D C N I T A D R K V Y P
TCAGAGATGGTGCCTGGCAGCGGTGACTGCAACATCACTGCCGACCGCAAGGTGTATCCA
|||||
TCAGAGATGGTGCCTGGCAGCGGTGACTGCAACATCACTGCCGACCGCAAGGTGTATCCA

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (241)
Lewis FT DNA

Q A D A V I V H H R E V M Y N P S A Q L
CAGCAGACGCGGTGATCGTGACACCGAGAGGTGATGTACAACCCAGTGCCTCAGCTC
|||||
CAGCAGACGCGGTGATCGTGACACCGAGAGGTGATGTACAACCCAGTGCCTCAGCTC

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (301)
Lewis FT DNA

P R S P R R Q G Q R W I W F S M E S P S
CCACGCTCCCGAGGCGGCGAGCGGATGATCTGGTTCAAGTGGAGTCCCCAAGC
|||||
CCACCTTCCCCGAGGCGGCGAGCGGCTGGATCTGGTTCAACTTGGAGCCACCCCT

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (361)
Lewis FT DNA

H C W Q L K A M D G Y F N L T M S Y R S
CACTGCTGGCAGCTGAAGCCATGGACGGATACTTCAATCTCACCATGTCTACCGCAGC
|||||
AACTGCCAGCACCTGGAAGCCCTGGACAGATACTTCAATCTCACCATGTCTACCGCAGC

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (421)
Lewis FT DNA

D S D I F T P Y G W L E P W S G Q P A H
GACTCCGACATCTTCACGCCCTACGGCTGGCTGGAGCCGTGGTCCGGCCAGCCTGCCAC
|||||
GACTCCGACATCTTCACGCCCTACGGCTGGCTGGAGCCGTGGTCCGGCCAGCCTGCCAC

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (481)
Lewis FT DNA

FIG. 7B

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (541)
Lewis FT DNA

P P L N L S A K T E L V A W A V S N W G
CCACCGCTCAACCTCTCGGCCAAGACCGAGCTGGTGGCCTGGCAGTGTCCAACTGGGGG
|||||
CCACCGCTCAACCTCTCGGCCAAGACCGAGCTGGTGGCCTGGCAGTGTCCAACTGGGAAG

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (601)
Lewis FT DNA

P N S A R V R Y Y Q S L Q A H L K V D V
CCAAACTCCGCCAGGTGGTGGTACTACTACAGAGCCTGCAGGCCCATCTCAAGGTGGACGTG
|||||
CCGGAATCAGCCAGGTGGTGGTACTACTACAGAGCCTGCAGGCTCATCTCAAGGTGGACGTG

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (661)
Lewis FT DNA

Y G R S H K P L P Q G T M E T L S R Y
TACGGACGCTCCACAAAGCCCTGCCCCAGGAACCATGATGGAGACGCTGTCCCGGTAC
|||||
TACGGACGCTCCACAAAGCCCTGCCCCAAGGGACCATGATGGAGACGCTGTCCCGGTAC

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (721)
Lewis FT DNA

K F Y L A F E N S L H P D Y I T E K L W
AAGTTCTATCTGGCCTTCGAGAACTCCTTGCAACCCCGACTACATCACCGAGAAGCTGTGG
|||||
AAGTTCTACCTGGCCTTCGAGAACTCCTTGCAACCCCGACTACATCACCGAGAAGCTGTGG

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (781)
Lewis FT DNA

R N A L E A W A V P V V L G P S R S N Y
AGGAACGCCCTGGAGGCCTGGGCCGTGGCCCGTGGTGGTGGCCCGCAGCAGAACTACTAC
|||||
AGGAACGCCCTGGAGGCCTGGGCCGTGGCCCGTGGTGGTGGCCCGCAGCAGAACTACTAC

FIG. 7C

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (841)
Lewis FT DNA

E R F L P P D A F I H V D D F Q S P K D
GAGAGTTCTGCTGACCCGACGCTTCCATCCAGTGGACGACTTCCAGAGCCCCAAGGAC
|||||
GAGAGTTCTGCTGACCCGACGCTTCCATCCAGTGGACGACTTCCAGAGCCCCAAGGAC

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (901)
Lewis FT DNA

L A R Y L Q E L D K D H A R Y L S Y F R
CTGGCCCGGTACTGCTGAGAGCTGGACAAGGACCAAGGACCCCGCTACCTGAGCTACTTTCGC
|||||
CTGGCCCGGTACTGCTGAGAGCTGGACAAGGACCAAGGACCCCGCTACCTGAGCTACTTTCGC

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (961)
Lewis FT DNA

W R E T L R P R S F S W A L A F C K A C
TGGCGGAGACGCTGGCGCCTCGCTCCTTCAAGTGGGCACTCGCTTCTGCAAGGCCTGC
|||||
TGGCGGAGACGCTGGCGCCTCGCTCCTTCAAGTGGGCACTCGCTTCTGCAAGGCCTGC

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (1021)
Lewis FT DNA

W K L Q E E S R Y Q T R G I A A W F T Stop
TGGAAACTGCAGGAGGAATCCAGGTACCAAGACACGCGGC...ATAGCGGCTTGGTTACCTGA
|||||
TGGAAACTGCAGGAGGAATCCAGGTACCAAGACGCGGTGCGCAGCATAGCGGCTTGGTTACCTGA

GAGGCTGGTGGGGCTGGGCTGCCAGGAACCTCATTTCTGGGGCTCACCTGAGTG
GGGCGCTCATCTAAGGACTCGTTTGCTGAAGCTTCACTGCTGAGGACTCACCT
GCTGGGACGGTCACTGTTGCAAGTTCACCTGCTGGGATTCACCTACCTGGTCCCTC
ACTTCTGGGGCTCACCTGCTGGAGTCTTGGTGGCCAGGATGTCCCTTACCTGGGA
TTTCAATGCTGGCTTCCAGGAGCGTCCCTGCGGAAGCCTGGCTGCTGGGATGTCTC
CTGGGACTTTCCTACTGGGACCTCGGCTGTTGGGACCTTACCTGCTGGGACCTGCT
CCCAGAGACCTTCCACACTGAATCTCACCTGTAGGAGCCTCACCTGCTGGGACCTCAC
CCTGGAGGCACTGGGGCTGGGAAC

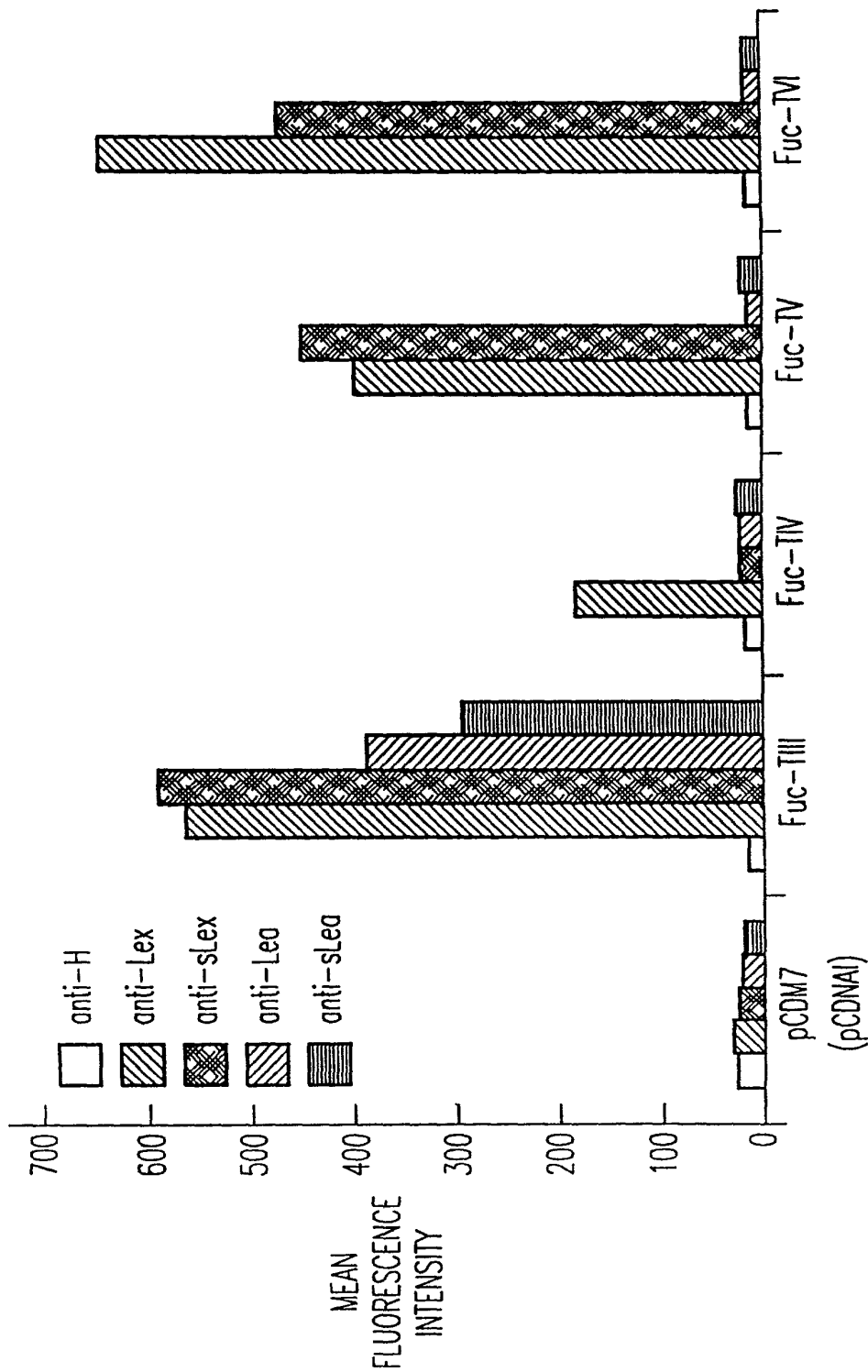


FIG. 8